



10077137 Sequence Listing  
SEQUENCE LISTING

<110> MACKAY, FABIENNE  
BROWNING, JEFFREY  
AMBROSE, CHRISTINE  
TSCHOPP, JURG  
SCHNEIDER, PASCAL  
THOMPSON, JEFFREY

<120> BAFF RECEPTOR (BCMA), AN IMMUNOREGULATORY AGENT

<130> 08201.0027

<140> 10/077,137

<141> 2002-02-15

<150> PCT/US00/22507

<151> 2000-08-16

<150> 60/149,378

<151> 1999-08-17

<150> 60/181,684

<151> 2000-02-11

<150> 60/183,536

<151> 2000-02-18

<160> 9

<170> PatentIn ver. 3.3

<210> 1

<211> 184

<212> PRT

<213> Homo sapiens

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Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser  
35 40 45

Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu  
50 55 60

Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile  
65 70 75 80

Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu  
85 90 95

Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu  
100 105 110

Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys  
115 120 125

Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe  
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Pro Leu Pro Ala Met	Glu Glu Gly Ala Thr	Ile Leu Val Thr Thr	Lys
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Ile Glu Lys Ser	Ile Ser Ala Arg		
	180		

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 gtaatgcaag tgtgaccaat tcagtgaag gaacgaatgc gattctctgg acctgtttgg 180  
 gactgagctt aataatttct ttggcagttt tcgtgctaata gtttttgcta aggaagataa 240  
 gctctgaacc attaaaggac gagtttaaaa acacaggatc aggtctcctg ggcatggcta 300  
 acattgacct ggaaaagagc aggactgggtg atgaaattat tctccgagag gcctcgagta 360  
 cacggtggaa gaatgcacct gtgaagactg catcaagagc aaaccgaagg tcgactctga 420  
 ccattgcttt ccactcccag ctatggagga aggcgcaacc attctgtcac cacgaaaacg 480  
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 tctgctaggt aa 552

<210> 3  
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 20 25 30  
 Asp Ser Leu Asp Val Thr Met Leu Gln Met Ala Gly Gln Cys Ser Gln  
 35 40 45  
 Asn Glu Tyr Phe Asp Ser Leu Leu His Ala Cys Ile Pro Cys Gln Leu  
 50 55 60  
 Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Leu His Ala Cys Ile  
 65 70 75 80  
 Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr Pro Pro Leu Thr Cys Gln  
 85 90 95  
 Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Gln Arg Tyr  
 100 105 110  
 Cys Asn Ala Ser Val Thr Asn Ser Val Lys Gly Val Asp Lys Thr His  
 115 120 125  
 Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val  
 130 135 140

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Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr  
 145 150 155 160  
 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu  
 165 170 175  
 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys  
 180 185 190  
 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Tyr Val Val Ser Val  
 195 200 205

<210> 4  
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 ttgcatgctt gcataacctg tcaacttcga tgttcttcta atactcctcc tctaaccatgt 180  
 cagcggttatt gtaatgcaag tgtgaccaat tcagtgaag gagtcgacaa aactcacaca 240  
 tgcccaccgt gccacgaccc tgaactcctg gggggaccgt cagtcttcct cttcccccca 300  
 aaaccaagg acaccctcat gatctcccgg acccctgagg tcacatgcgt ggtggtggac 360  
 gtgagccacg aagaccctga ggtcaagttc aactgggtacg tggacggcgt ggaggtgcat 420  
 aatgccaaga caaagccgcg ggaggagcag tacaacagca cgtaccgtgt ggtcagcgtc 480  
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 Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
 35 40 45  
 Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val  
 50 55 60  
 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
 65 70 75 80  
 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp  
 85 90 95  
 Gly Ser Phe Phe Lys Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
 100 105 110  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
 115 120 125  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 130 135 140

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 <212> DNA  
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 acctgcctgg tcaaaggctt ctatcccagc gacatcgccg tggagtggga gagcaatggg 180  
 cagccggaga acaactacaa gaccacgcct cccgtgttgg actccgacgg ctcttcttc 240  
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<400> 7  
 Met Leu Gln Met Ala Gly Gln Cys Ser Gln Asn Glu Tyr Phe Asp Ser  
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 Leu Leu His Ala Cys Ile Pro Cys Gln Leu Arg Cys Ser Ser Asn Thr  
 20 25 30  
 Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser  
 35 40 45  
 Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu  
 50 55 60  
 Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile  
 65 70 75 80  
 Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu  
 85 90 95  
 Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu  
 100 105 110  
 Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys  
 115 120 125  
 Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe  
 130 135 140  
 Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys  
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 165 170 175  
 Ile Glu Lys Ser Ile Ser Ala Arg  
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gctcccaaaa tgaatatattt gacagtttgt tgcagtcttg cataccttgt caacttcgat 300
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<210> 9
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          20          25          30
Arg Lys Glu Ser Pro Ser Val Arg Ser Ser Lys Asp Gly Lys Leu Leu
          35          40          45
Ala Ala Thr Leu Leu Leu Ala Leu Leu Ser Cys Cys Leu Thr Val Val
          50          55          60
Ser Phe Tyr Gln Val Ala Ala Leu Gln Gly Asp Leu Ala Ser Leu Arg
          65          70          75          80
Ala Glu Leu Gln Gly His His Ala Glu Lys Leu Pro Ala Gly Ala Gly
          85          90          95
Ala Pro Lys Ala Gly Leu Glu Glu Ala Pro Ala Val Thr Ala Gly Leu
          100          105          110
Lys Ile Phe Glu Pro Pro Ala Pro Gly Glu Gly Asn Ser Ser Gln Asn
          115          120          125
Ser Arg Asn Lys Arg Ala Val Gln Gly Pro Glu Glu Thr Val Thr Gln
          130          135          140
Asp Cys Leu Gln Leu Ile Ala Asp Ser Glu Thr Pro Thr Ile Gln Lys
          145          150          155          160
Gly Ser Tyr Thr Phe Val Pro Trp Leu Leu Ser Phe Lys Arg Gly Ser
          165          170          175
Ala Leu Glu Glu Lys Glu Asn Lys Ile Leu Val Lys Glu Thr Gly Tyr
          180          185          190

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Phe	Phe	Ile	Tyr	Gly	Gln	Val	Leu	Tyr	Thr	Asp	Lys	Thr	Tyr	Ala	Met
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	210					215					220				
Ser	Leu	Val	Thr	Leu	Phe	Arg	Cys	Ile	Gln	Asn	Met	Pro	Glu	Thr	Leu
225					230					235					240
Pro	Asn	Asn	Ser	Cys	Tyr	Ser	Ala	Gly	Ile	Ala	Lys	Leu	Glu	Glu	Gly
				245					250					255	
Asp	Glu	Leu	Gln	Leu	Ala	Ile	Pro	Arg	Glu	Asn	Ala	Gln	Ile	Ser	Leu
			260					265					270		
Asp	Gly	Asp	Val	Thr	Phe	Phe	Gly	Ala	Leu	Lys	Leu	Leu			
		275					280					285			